

WO 99/64607

PCT/FR99/01343

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LIST OF SEQUENCES

(iii) NUMBER OF SEQUENCES: 4

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTCCTG TTGACAATTA ATCATCGAAC TAGTTAACTA GTACGCAGCT TGGCTGCAGG	60
TCGACCTGCA GCCAAGCTTG GGCATACATT CAATCAATTG TTATCTAAGG AAATACTTAC	120
A	121

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1793 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20 (ix) CHARACTERISTIC:

- (A) NAME/KEY: CDS
 (B) POSITION: 123..1190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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GAATTCCTG TTGACAATTA ATCATCGAAC TAGTTAACTA GTACGCAGCT TGGCTGCAGG	60
TCGACCTGCA GCCAAGCTTG GGCATACATT CAATCAATTG TTATCTAAGG AAATACTTAC	120
AT ATG CAG ACA AGA AAA ATC GTC CGG GCA GCC GCC GTA CAG GCC GCC	167
Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala	
1 5 10 15	
TCT CCC AAC TAC GAT CTG GCA ACG GGT GTT GAT AAA ACC ATT GAG CTG	215
Ser Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu	
20 25 30	
GCT CGT CAG GCC CGC GAT GAG GGC TGT GAC CTG ATC GTG TTT GGT GAA	263
Ala Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu	
35 40 45	
ACC TGG CTG CCC GGC TAT CCC TTC CAC GTC TGG CTG GGC GCA CCG GCC	311
Thr Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala	
50 55 60	

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TGG TCG CTG AAA TAC AGT GCC CGC TAC TAT GCC AAC TCG CTC TCG CTG	359
Trp Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu	
65 70 75	
GAC AGT GCA GAG TTT CAA CGC ATT GCC CAG GCC GCA CGG ACC TTG GGT	407
Asp Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly	
80 85 90 95	
ATT TTC ATC GCA CTG GGT TAT AGC GAG CGC AGC GGC GGC AGC CTT TAC	455
Ile Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr	
100 105 110	
CTG GGC CAA TGC CTG ATC GAC GAC AAG GGC CAG ATG CTG TGG TCG CGT	503
Leu Gly Gln Cys Leu Ile Asp Asp Lys Gly Gln Met Leu Trp Ser Arg	
115 120 125	
CGC AAA CTC AAA CCT ACA CAT GTT GAG CGC ACC GTG TTT GGT GAA GGT	551
Arg Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly	
130 135 140	
TAT GCC CGA GAT CTG ATT GTG TCC GAC ACC GAG CTG GGC CGC GTC GGT	599
Tyr Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly	
145 150 155	
GCC CTG TGC TGC TGC GAG CAC CTG TCC CCC TTG AGC AAG TAC GGC CTG	647
Ala Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu	
160 165 170 175	
TAC TCC CAG CAC GAA GCC ATT CAC ATT GCC GCC TGG CCG TCC TTT TCG	695
Tyr Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser	
180 185 190	
CTG TAC AGC GAA CAG GCC CAT GCG CTC AGC GCC AAG GTG AAC ATG GCT	743
Leu Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala	
195 200 205	
GCC TCG CAA ATC TAT TCG GTT GAA GGC CAG TGC TTT ACC ATC GCC GCC	791
Ala Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala	
210 215 220	
AGC AGT GTC GTC ACC CAG GAG ACA CTG GAC ATG CTG GAA GTA GGT GAA	839
Ser Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu	
225 230 235	
CAC AAC GCC TCC CTG CTG AAA GTG GGC GGC GGC AGT TCC ATG ATT TTT	887
His Asn Ala Ser Leu Leu Lys Val Gly Gly Gly Ser Ser Met Ile Phe	
240 245 250 255	
GCG CCG GAC GGA CGC ACA TTG GCT CCC TAC CTG CCA CAC GAT GCC GAA	935
Ala Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu	
260 265 270	
GGC CTG ATC ATT GCC GAT CTG AAC ATG GAA GAA ATT GCC TTC GCC AAG	983
Gly Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys	
275 280 285	
GCG ATC AAC GAC CCT GTG GGC CAC TAC TCC AAA CCC GAG GCC ACC CGT	1031
Ala Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg	
290 295 300	

REPLACEMENT SHEET (RULE 26)

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CTG GTA CTG GAC CTG GGG CAC CGT GAG CCC ATG ACT CGG GTG CAT TCC	1079
Leu Val Leu Asp Leu Gly His Arg Glu Pro Met Thr Arg Val His Ser	
305 310 315	
AAA AGC GTG ATC CAG GAA GAA GCT CCC GAG CCG CAC GTG CAA AGT ACG	1127
Lys Ser Val Ile Gln Glu Glu Ala Pro Glu Pro His Val Gln Ser Thr	
320 325 330 335	
GCT GCG CCC GTC GCC GTC AGC CAG ACT CAG GAC TCG GAT ACG CTA CTG	1175
Ala Ala Pro Val Ala Val Ser Gln Thr Gln Asp Ser Asp Thr Leu Leu	
340 345 350	
GTG CAA GAA CCG TCC TGA CCCCCAAAAGA TGACAAGGCC CGGGCAAAT	1223
Val Gln Glu Pro Ser	
355	
GTCCGGGTCT TGATTCCTTC TCGTCCCGG ATCCACTAGT TCTAGAGTCG ACCTGCAGGC	1283
ATGCAAGCTT GGGTCCCACC TGACCCCATG CCGAACTCAG AAGTGAAACG CCGTAGCGCC	1343
GATGCTAGTG TGGGGTCTCC CCATGCGAGA GTAGGGAAGT GCCAGGCATC AAATAAAACG	1403
AAAGGCTCAG TCGAAAGACT GGGCCTTTTCG TTTTATCTGT TGTTTGTTCG TGAACGCTCT	1463
CCTGAGTAGG ACAAATCCGC CGGGAGCGGA TTTGAACGTT GCGAAGCAAC GGCCCGGAGG	1523
GTGGCGGGCA GGACGCCCCG CATAAACTGC CAGGCATCAA ATTAAGCAGA AGGCCATCCT	1583
GACGGATGGC CTTTTTTCGT TTCTACAAAC TCTTCCTGTC GTCATATCTA CAAGCCATCC	1643
CCCCACAGAT ACGGTAACT AGCCTCGTTT TTGCATCAGG AAAGCAGCTA TGAACCACTC	1703
CTTAAACCC TGGAACACAT TTGGCATTGA TCATAATGCT CAGCACATTG TATGTGCCGA	1763
AGACGAACAA CAATTACTCA ATGCCCCGCG	1793

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 35 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCCCCGACA GCTGTCTTGC TTTCGAATTT CTGCC

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleotide

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TTGACGTCAG TAGCTGAACA GGAGGG

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